

Blast SEQ ID NO:1 versus human genomic

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
44,521 sequences; 200,768,834,160 total letters

Query= LEX161seqid1
(2115 letters)

Score	E
(bits)	

Sequences producing significant alignments:

Value

AC016643.6.1.179969	<u>734</u>	0.0
AC008958.7.1.109526	<u>520</u>	e-
144		

>AC016643.6.1.179969
Length = 179969

Score = 734 bits (370), Expect = 0.0.

Identities = 370/370 (100%)

Strand = Plus / Plus

Query: 957 agatgatttaagccagaagttaaaacccttgggtgaaggcagaacgagagttttttgaa
1016 |||||||

Sbjct: 60550 agatgatttaagccagaagttaaaacccttgggtgaaggcagaacgagagttttttgaa
60609 |||||||

Query: 1017 tttgaagaaaaaggaatgcaaagacaggggtttgaatatgatggaaaatcaatgcctg
1076 |||||||

Sbjct: 60610 tttgaagaaaaaggaatgcaaagacaggggtttgaatatgatggaaaatcaatgcctg
60669 |||||||

Query: 1077 ggatctatattactacatgactcagacagaggaactcaagtattccatagaccaagagtt
1136 |||||||

Sbjct: 60670 ggatctatattactacatgactcagacagaggaactcaagtattccatagaccaagagtt
60729 |||||||

Query: 1137 cctcaaggaatacttccaattgaggtggtcactgaaggcttgctgaacacacctaccagga
1196 |||||||

Sbjct: 60730 cctcaaggaatacttccaattgaggtggtcactgaaggcttgctgaacacacctaccagga
60789 |||||||

Query: 1197 gttgttggacttcattgaacaaatgacagatgctcatgttggacaagaagagtgtac.
1256 |||||||
Sbjct: 60790 gttgttggacttcattgaacaaatgacagatgctcatgttggacaagaagagtgtac
60849

Query: 1257 actttatactgtgaaggataaagctacaggagaagtattggacagttctattggacct
1316 |||||||
Sbjct: 60850 actttatactgtgaaggataaagctacaggagaagtattggacagttctattggacct
60909

Query: 1317 ctatccaagg 1326
|||||||
Sbjct: 60910 ctatccaagg 60919

Score = 520 bits (262), Expect = e-144
Identities = 262/262 (100%)
Strand = Plus / Plus

Query: 40 agagttggtggtccaggatttactcagaatgacgttaggaagagaagtgtatgtccct
99 |||||||
Sbjct: 30994 agagttggtggtccaggatttactcagaatgacgttaggaagagaagtgtatgtccct
31053

Query: 100 cttcaggcaatgtcttccatactgtggctggcagaaatgtttaagatggatcttca
159 |||||||
Sbjct: 31054 cttcaggcaatgtcttccatactgtggctggcagaaatgtttaagatggatcttca
31113

Query: 160 ccagagcaaattaaaacaagaactgaggagctattgtcagaccaaacaggtgtacgt
219 |||||||
Sbjct: 31114 ccagagcaaattaaaacaagaactgaggagctattgtcagaccaaacaggtgtacgt
31173

Query: 220 gctgttggaatgctcggtattgaggaacttacgagaactgtctgcaggcactggca
279 |||||||
Sbjct: 31174 gctgttggaatgctcggtattgaggaacttacgagaactgtctgcaggcactggca
31233

Query: 280 gatgtagaagtaaagtatata 301
|||||||
Sbjct: 31234 gatgtagaagtaaagtatata 31255

Score = 405 bits (204), Expect = e-110

Identities = 204/204 (100%)
Strand = Plus / Plus

Query: 1324 aggaaaggaaaatacatcatgcggcctgcttcggtccagcctggctgccttctgcct
1383 |||||||

Sbjct: 64886 aggaaaggaaaatacatcatgcggcctgcttcggtccagcctggctgccttctgcct
64945 |||||||

Query: 1384 gatggaagccggatgtggcagtggctgcctcgtaacttctcacagccagtggca
1443 |||||||

Sbjct: 64946 gatggaagccggatgtggcagtggctgcctcgtaacttctcacagccagtggca
65005 |||||||

Query: 1444 ggtcgccctctcctgagacacgacgagggtgaggacttactttcatgagttggcac
1503 |||||||

Sbjct: 65006 ggtcgccctctcctgagacacgacgagggtgaggacttactttcatgagttggcac
65065 |||||||

Query: 1504 gtgatgcatcagatttgtgcacag 1527

Sbjct: 65066 gtgatgcatcagatttgtgcacag 65089 |||||||

Score = 379 bits (191), Expect = e-102

Identities = 191/191 (100%)

Strand = Plus / Plus

Query: 1526 agactgatttgacgatttagcggAACAAATGTGGAAACTGACTTTTAGAGGTCAC
1585 |||||||

Sbjct: 81947 agactgatttgacgatttagcggAACAAATGTGGAAACTGACTTTTAGAGGTCAC
82006 |||||||

Query: 1586 cgcaaATGCTTGAATTGGGTGTGGGACGTCGATTCCCTCCGAAGATTGTCAAAACATT
1645 |||||||

Sbjct: 82007 cgcaaATGCTTGAATTGGGTGTGGGACGTCGATTCCCTCCGAAGATTGTCAAAACATT
82066 |||||||

Query: 1646 ataaAGATGGAAGCCATTGAGACGATCTGCTTGAACACTTGTGCTTAGGCTGG
1705 |||||||

Sbjct: 82067 ataaAGATGGAAGCCATTGAGACGATCTGCTTGAACACTTGTGCTTAGGCTGG
82126 |||||||

Query: 1706 tcaacacaggt 1716

Sbjct: 82127 tcaacacaggt 82137 |||||||

Score = 323 bits (163), Expect = 2e-85
Identities = 163/163 (100%)
Strand = Plus / Plus

Query: 661 ggtgctttcctgatgattcattgacagtttagaaaagacagatgatgacaagtataaa
720 |||||||
Sbjct: 53694 ggtgctttcctgatgattcattgacagtttagaaaagacagatgatgacaagtataaa
53753

Query: 721 attacctaaaaatccacactatccctgtcatgaagaaatgttgtatccctgaaacc
780 |||||||
Sbjct: 53754 attacctaaaaatccacactatccctgtcatgaagaaatgttgtatccctgaaacc
53813

Query: 781 agaagaaggatggaaatggctttaatacaaggtgcaaagagg 823
|||
Sbjct: 53814 agaagaaggatggctttaatacaaggtgcaaagagg 53856

Score = 301 bits (152), Expect = 8e-79
Identities = 152/152 (100%)
Strand = Plus / Plus

Query: 300 agtgaaaggaccatgctagacttccccagcatgtatcctctgacaaagaagtacgac
359 |||||||
Sbjct: 35386 agtgaaaggaccatgctagacttccccagcatgtatcctctgacaaagaagtacgac
35445

Query: 360 agcaagtacagaaggcagacaaaagactttctcgaaaaatggatattgagatgagcatgagagg
419 |||||||
Sbjct: 35446 agcaagtacagaaggcagacaaaagactttctcgaaaaatggatattgagatgagcatgagagg
35505

Query: 420 agatataattgagagaattgttcatggagg 451
|||
Sbjct: 35506 agatataattgagagaattgttcatggagg 35537

Score = 280 bits (141), Expect = 3e-72
Identities = 141/141 (100%)
Strand = Plus / Plus

Query: 1842 aggcacaaaatgccagctacccggacattggcagggggatacgatggccaatatta
1901 |||||||

Sbjct: 84687 aggcacaaaatgccagctaccttggacattttggcaggggatacgatggccaaatatta
84746

Query: 1902 tggatatcttggagtgaagtatttccatggatatgtttacagctgtttaaaaaga
1961

Sbjct: 84747 tggatatctttggagtgaagtatccatggatatgtttacagctttaaaaaga
84806

Query: 1962 agggataatgaatccagaggt 1982

Sbjct: 84807 agggataatgaatccagagg 84827

Score = 270 bits (136), Expect = 3e-69

Identities = 137/138 (99%)

Strand = Plus / Plus

Query: 821 agaaaaacaccataatttgcagcagctactcccactgcgaaccaagggtggccaaactac
880

Sbjct: 58207 agaaaaacaccataatttgcagcactccactgcgaaccaaggtgccaaactac
58266

Query: 881 tcggttatagcacacatgctactcgcccttgaatgaacactgcaaagagcacaagcc
940

Sbjct: 58267 tcggttatagcacacatgctgacttcgtccttgaatgaacactgcaaagagcacaaggcc
58326

Query: 941 gcgttaacagcyttctag 958

Query: mix grogan by -

Sbjct: 58327 gcgttaacagcctttctag 58344

Score = 268 bits (135), Expect = 1e-68

Identities = 136/137 (99%)

Strand = Plus / Plus

Query: 1979 aggttggaaatgaaaatacagaaacctaattccctggggatctctggacggatgg
2038

Sbjct: 95214 aggttggaaatgaaatacagaaaacctaattcctgaaacacctggggatctctggacggcatgg
95273

Query: 2039 acatgctccacaatttcttggaaacgtgagccaaacccaaaagcgttcctaattggatggag
2088

2098 Sbjct: 95274 acatgctccacaatttcttggaaacgtgagccaaaccaaaaagcgttcctaattgagttagag
2099

Query: 2099 gcctgcatgctycgtga 2115
||||||| |||||
Sbjct: 95334 gcctgcatgctccgtga 95350

Score = 262 bits (132), Expect = 7e-67
Identities = 132/132 (100%)
Strand = Plus / Plus

Query: 1713 aggtttctgaccctgcgccagattgtttgagcaaaggatcagtctcttcataccaa
1772 |||||||
Sbjct: 82469 aggtttctgaccctgcgccagattgtttgagcaaaggatcagtctcttcataccaa
82528

Query: 1773 cacatcgctggatgctgcaagtgaatatgccaaatactgctcagaaatattaggagttgc
1832 |||||||
Sbjct: 82529 cacatcgctggatgctgcaagtgaatatgccaaatactgctcagaaatattaggagttgc
82588

Query: 1833 agctactccagg 1844
|||||||
Sbjct: 82589 agctactccagg 82600

Score = 222 bits (112), Expect = 6e-55.
Identities = 116/117 (99%), Gaps = 1/117 (0%)
Strand = Plus / Plus

Query: 443 atttacagggaaacctgtgatctgggaaagataaaacctgaggccagacgatacttgaaaa
502 |||||
Sbjct: 49854 attt-cagggaaacctgtgatctgggaaagataaaacctgaggccagacgatacttgaaaa
49912

Query: 503 agtcaattaaaatggggaaaagaaatgggctccatcttcctgaacaagtacagaatg 559
|||||||
Sbjct: 49913 agtcaattaaaatggggaaaagaaatgggctccatcttcctgaacaagtacagaatg
49969

Score = 208 bits (105), Expect = 1e-50
Identities = 105/105 (100%)
Strand = Plus / Plus

Query: 559 gaaatcaaattaatgaagaaaagaatgagtgagctatgtattgatttaacaaaaacctc
618 |||||
Sbjct: 52613 gaaatcaaattaatgaagaaaagaatgagtgagctatgtattgatttaacaaaaacctc
52672

Query: 619 aatgaggatgatacttccctgtatTTCCAAGGCTGAACTTGGT 663
||| ||| ||| ||| ||| ||| |||
Sbjct: 52673 aatgaggatgatacTTCCCTGTATTTCCAAGGCTGAACTTGGT 52717

>AC008958.7.1.109526
Length = 109526
Score = 520 bits (262), Expect = e-144
Identities = 262/262 (100%)
Strand = Plus / Minus

Query: 40 agagttgggtggccaggatttactcagaatgacgttaggaagagaagtgtatgtctcct
99 ||| ||| ||| ||| ||| ||| |||
Sbjct: 24199 agagttgggtggccaggatttactcagaatgacgttaggaagagaagtgtatgtctcct
24140

Query: 100 cttcaggcaatgtcttcctatactgtggctggcagaaatgttttaagatggatctttca
159 ||| ||| ||| ||| ||| ||| |||
Sbjct: 24139 cttcaggcaatgtcttcctatactgtggctggcagaaatgttttaagatggatctttca
24080

Query: 160 ccagagcaaattaaaacaagaactgaggagctcattgtgcagaccaaacaggtgtacgt
219 ||| ||| ||| ||| ||| ||| |||
Sbjct: 24079 ccagagcaaattaaaacaagaactgaggagctcattgtgcagaccaaacaggtgtacgt
24020

Query: 220 gctgttggaatgctcggtattgaggaagtaacttacgagaactgtctgcaggcactggca
279 ||| ||| ||| ||| ||| ||| |||
Sbjct: 24019 gctgttggaatgctcggtattgaggaagtaacttacgagaactgtctgcaggcactggca
23960

Query: 280 gatgtagaagtaaaagtatata 301
||| ||| ||| |||
Sbjct: 23959 gatgtagaagtaaaagtatata 23938

Score = 323 bits (163), Expect = 2e-85
Identities = 163/163 (100%)
Strand = Plus / Minus

Query: 661 ggtgctttccctgtatgtttcattgacagtttagaaaagacagatgtacaagtataaa
720 ||| ||| ||| ||| ||| |||
Sbjct: 1504 ggtgctttccctgtatgtttcattgacagtttagaaaagacagatgtacaagtataaa
1445

Query: 721 attacctaaaatccacactattccctgtcatgaagaatgttcatccctgaaacc
780 |||||||
Sbjct: 1444 attacctaaaatccacactattccctgtcatgaagaatgttcatccctgaaacc
1385

Query: 781 agaagaaggatggaaatggcttaatacaaggtgcaaagagg 823
|||
Sbjct: 1384 agaagaaggatggcttaatacaaggtgcaaagagg 1342

Score = 301 bits (152), Expect = 8e-79
Identities = 152/152 (100%)
Strand = Plus / Minus

Query: 300 agtgaaaggaccatgctagactttccccagcatgtatcctctgacaaagaagtacgagc
359 |||||||
Sbjct: 19806 agtgaaaggaccatgctagactttccccagcatgtatcctctgacaaagaagtacgagc
19747

Query: 360 agcaagtacagaaggcagacaaaagactttctcgaaaaatggatattgagatgagcatgagagg
419 |||||||
Sbjct: 19746 agcaagtacagaaggcagacaaaagactttctcgaaaaatggatattgagatgagcatgagagg
19687

Query: 420 agatataatttggagagaattgttcatttacagg 451
|||||
Sbjct: 19686 agatataatttggagagaattgttcatttacagg 19655

Score = 222 bits (112), Expect = 6e-55
Identities = 116/117 (99%), Gaps = 1/117 (0%)
Strand = Plus / Minus

Query: 443 atttacaggaaacctgtgatctggggaaagataaaacctgaggccagacgataacttggaaa
502 |||||
Sbjct: 5344 attt-caggaaacctgtgatctggggaaagataaaacctgaggccagacgataacttggaaa
5286

Query: 503 agtcaattaaaatggggaaaagaaaatgggctccatttcctgaacaagtacagaatg 559
|||||
Sbjct: 5285 agtcaattaaaatggggaaaagaaaatgggctccatttcctgaacaagtacagaatg 5229

Score = 208 bits (105), Expect = 1e-50
Identities = 105/105 (100%)
Strand = Plus / Minus

Query: 559 gaaatcaaataaatgaagaaaagaatgagttagctatgtattgatttaacaaaacctc
618 |||||||

Sbjct: 2585 gaaatcaaataaatgaagaaaagaatgagttagctatgtattgatttaacaaaacctc
2526 |||||||

Query: 619 aatgaggatgatacccttccttgcattttccaaggctgaacttggt 663
|||||||

Sbjct: 2525 aatgaggatgatacccttccttgcattttccaaggctgaacttggt 2481
|||||||

Score = 81.8 bits (41), Expect = 2e-12

Identities = 41/41 (100%)

Strand = Plus / Minus

Query: 1 atgatcgccccgggtgcctttggctgtgcgaaggcctccgcag 41
|||||||

Sbjct: 60390 atgatcgccccgggtgcctttggctgtgcgaaggcctccgcag 60350
|||||||